

SEQUENCE LISTING

(1) GENERAL INFORMATION:

T, 4150
F²
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(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

(iii) NUMBER OF SEQUENCES: 273

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/470,896
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(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 7872-020

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15

Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30

Trp Asn Trp Phe
 35

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Ser Glu Ser Phe Thr Leu Leu Glu Gln Trp Asn Asn Trp Lys Leu
 1 5 10 15

Gln Leu Ala Glu Gln Trp Leu Glu Gln Ile Asn Glu Lys His Tyr Leu
 20 25 30

Glu Asp Ile Ser
 35

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Thr Asn Thr Ile Tyr Thr Leu Leu Glu Glu Ser Gln Asn Gln Gln
 1 5 10 15

Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30

Trp Asn Trp Phe
 35

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Tyr Thr Gly Ile Ile Tyr Asn Leu Leu Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Asn Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Thr Ser Leu Ile Tyr Ser Leu Leu Glu Lys Ser Gln Thr Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Glu Ala Asn Ile Ser Lys Ser Leu Glu Gln Ala Gln Ile Gln Gln
1 5 10 15
Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp Asp Ile Phe
20 25 30
Gly Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Glu Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln
1 5 10 15
Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp Asp Val Phe
20 25 30
Thr Asn Trp Leu
35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Gly Gly Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu
1 5 10 15
Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu
20 25 30
Ala Val Glu Arg Tyr Leu Lys Asp Gln
35 40

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln
1 5 10 15
Gln

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln Glu Met Leu Arg Leu
1 5 10 15
Thr Val Trp Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu
20 25 30
Lys Tyr Leu Lys Asp Gln
35

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGACGCTGA CGGTACAGGC C

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGACTAAGCT TAATACCACA GCCAATTTGT TAT

33

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGCTGCTT GGGGCCCCAG AC

22

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCAAATCCCC AGGAGCTGCT CGAGCTGCAC TATACCAGAC

40

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATAGCTTCTA GATTAATTGT TAATTTCTCT GTCCC

35

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys
 1 5 10 15
 Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp
 20 25 30
 Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile
 1 5 10 15
 Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys
 20 25 30
 Ser Asp Glu Leu Leu
 35

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a

9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile Thr Leu Asn Asn Ser Val Ala Leu Asp Pro Ile Asp Ile Ser Ile
1 5 10 15

Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile
20 25 30

Arg Arg Ser
35

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
1 5 10 15

Val Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala
20 25 30

Ile Arg

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile
1				5					10					15	

Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
			20				25						30		

Ser

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala
 1 5 10 15
 Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser
 20 25 30
 Val

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu
 1 5 10 15
 Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val
 20 25 30
 Leu

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular

carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu Leu
1 5 10 15

Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu
20 25 30

Thr

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu Leu Ser
1 5 10 15

Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr
20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala
1				5					10					15	
Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu
			20					25					30		

Asp

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Glu Val Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val

1	5	10	15
Ser	Leu	Ser	Asn
Gly	Val	Ser	Val
Leu	Thr	Ser	Lys
Val	Leu	Asp	Leu
20	25	30	

Lys

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser
1				5					10					15	
Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys
			20					25					30		

Asn

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu
1 5 10 15

Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn
20 25 30

Tyr

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser
1 5 10 15

Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
20 25 30

Ile

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn
1				5					10					15	

Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile
			20					25					30		

Asp

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly
1				5					10					15	

Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Lys

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
1				5					10					15	

Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys
			20					25					30		

Gln

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 48
(D) OTHER INFORMATION: /label= B
/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Thr Leu Asn Asn Ser Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu
1 5 10 15
Leu Asn Lys Ala Lys Ser Asp Leu Glu Ser Lys Glu Trp Ile Arg
20 25 30
Arg Ser Asn
35

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Asn Asn Ser Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu
1 5 10 15
Asn Lys Ala Lys Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg
20 25 30
Ser Asn Gln
35

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asn	Asn	Ser	Val	Ala	Leu	Asp	Pro	Ile	Asp	Ile	Ser	Ile	Glu	Leu	Asn
1				5				10					15		
Lys	Ala	Lys	Ser	Asp	Leu	Glu	Glu	Ser	Lys	Glu	Trp	Ile	Arg	Arg	Ser
		20					25						30		
Asn	Gln	Lys													
		35													

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asn	Ser	Val	Ala	Leu	Asp	Pro	Ile	Asp	Ile	Ser	Ile	Glu	Leu	Asn	Lys
1				5				10					15		
Ala	Lys	Ser	Asp	Leu	Glu	Glu	Ser	Lys	Glu	Trp	Ile	Arg	Ser	Asn	
		20					25					30			

Gln Lys Leu
35

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser	Val	Ala	Leu	Asp	Pro	Ile	Asp	Ile	Ser	Ile	Glu	Leu	Asn	Lys	Ala
1				5				10						15	
Lys	Ser	Asp	Leu	Glu	Glu	Ser	Lys	Glu	Trp	Ile	Arg	Arg	Ser	Asn	Gln
			20					25					30		
Lys	Leu	Asp													
			35												

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys
1           5           10           15
Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys
          20           25           30
Leu Asp Ser
          35
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser
1           5           10           15
Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu
          20           25           30
Asp Ser Ile
          35
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp
1 5 10 15

Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp
20 25 30

Ser Ile Gly
35

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu
1 5 10 15

Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser
20 25 30

Ile Gly Asn

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu
 1             5             10             15

Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile
      20             25             30

Gly Asn Trp
      35

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl

group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu
1           5           10           15

Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile Gly
          20           25           30

Asn Trp His
          35
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu Ser
1           5           10           15

Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile Gly Asn
          20           25           30

Trp His Gln
          35
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A
 /note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ile	Ser	Ile	Glu	Leu	Asn	Lys	Ala	Lys	Ser	Asp	Leu	Glu	Glu	Ser	Lys
1				5					10					15	
Glu	Trp	Ile	Arg	Arg	Ser	Asn	Gln	Lys	Leu	Asp	Ser	Ile	Gly	Asn	Trp
			20					25					30		
His	Gln	Ser													
			35												

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A
 /note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser	Ile	Glu	Leu	Asn	Lys	Ala	Lys	Ser	Asp	Leu	Glu	Glu	Ser	Lys	Glu
1				5					10					15	
Trp	Ile	Arg	Arg	Ser	Asn	Gln	Lys	Leu	Asp	Ser	Ile	Gly	Asn	Trp	His
			20					25					30		
Gln	Ser	Ser													
			35												

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu Ser Lys Glu Trp
1 5 10 15

Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile Gly Asn Trp His Gln
20 25 30

Ser Ser Thr
35

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile
1 5 10 15
Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile Gly Asn Trp His Gln Ser
20 25 30
Ser Thr Thr
35

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Thr Ala Ala Val Ala Leu Val Glu Ala Lys Gln Ala Arg Ser Asp Ile
1 5 10 15
Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser
20 25 30
Val Gln Ser
35

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
Ala Val Ala Leu Val Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys
1           5           10           15
Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln
20           25           30
Ser Ser Ile
35
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Leu Val Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu
1           5           10           15
Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile
20           25           30
Gly Asn Leu
35
```

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala
1 5 10 15

Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly
20 25 30

Asn Leu Ile
35

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile
1 5 10 15
Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly Asn
20 25 30
Leu Ile Val
35

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg
1 5 10 15
Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu
20 25 30
Ile Val Ala
35

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group,

a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg Asp
 1             5             10             15
Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu Ile
      20             25             30
Val Ala Ile
      35
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr
 1             5             10             15
Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu Ile Val
      20             25             30
Ala Ile Lys
      35
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala	Arg	Ser	Asp	Ile	Glu	Lys	Leu	Lys	Glu	Ala	Ile	Arg	Asp	Thr	Asn
1				5					10					15	

Lys	Ala	Val	Gln	Ser	Val	Gln	Ser	Ser	Ile	Gly	Asn	Leu	Ile	Val	Ala
			20					25					30		

Ile	Lys	Ser
		35

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys
 1 5 10 15
 Ala Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu Ile Val Ala Ile
 20 25 30
 Lys Ser Val
 35

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala
 1 5 10 15
 Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu Ile Val Ala Ile Lys
 20 25 30
 Ser Val Gln
 35

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular

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carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val
 1              5              10              15
Gln Ser Ser Ile Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln Asp
          20              25              30
Tyr Val Asn
          35
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln
 1              5              10              15
Ser Ser Ile Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln Asp Tyr
          20              25              30
Val Asn Lys
          35
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile
1 5 10 15

Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln Asp Tyr Val Asn Lys
20 25 30

Glu Ile Val
35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Trp Gln Glu Trp Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr

1	5	10	15
Ala	Leu	Leu	Glu
	20	Glu	Ala
		Gln	Ile
		25	Gln
		Gln	Glu
		Lys	Asn
			Met
			30
			Tyr
			Glu
Leu	Gln	Lys	
	35		

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gln	Glu	Trp	Glu	Arg	Lys	Val	Asp	Phe	Leu	Glu	Glu	Asn	Ile	Thr	Ala
1				5					10					15	
Leu	Leu	Glu	Glu	Ala	Gln	Ile	Gln	Gln	Glu	Lys	Asn	Met	Tyr	Glu	Leu
		20					25						30		
Gln	Lys	Leu													
		35													

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Glu Trp Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu
1 5 10 15

Leu Glu Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln
20 25 30

Lys Leu Asn
35

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Trp Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu
1 5 10 15

Glu Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys
20 25 30

Leu Asn Ser
35

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Glu	Arg	Lys	Val	Asp	Phe	Leu	Glu	Glu	Asn	Ile	Thr	Ala	Leu	Leu	Glu
1				5					10					15	

Glu	Ala	Gln	Ile	Gln	Gln	Glu	Lys	Asn	Met	Tyr	Glu	Leu	Gln	Lys	Leu
			20					25					30		

Asn	Ser	Trp
		35

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Arg	Lys	Val	Asp	Phe	Leu	Glu	Glu	Asn	Ile	Thr	Ala	Leu	Leu	Glu	Glu
1				5					10					15	

Ala	Gln	Ile	Gln	Gln	Glu	Lys	Asn	Met	Tyr	Glu	Leu	Gln	Lys	Leu	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser Trp Asp
35

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu Glu Ala
1 5 10 15

Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser
20 25 30

Trp Asp Val
35

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu Glu Ala Gln
 1              5              10              15

Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp
          20              25              30

Asp Val Phe
          35
  
```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu Glu Ala Gln Ile
 1              5              10              15

Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp Asp
          20              25              30

Val Phe Gly
          35
  
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A
 /note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Phe	Leu	Glu	Glu	Asn	Ile	Thr	Ala	Leu	Leu	Glu	Glu	Ala	Gln	Ile	Gln
1				5				10						15	
Gln	Glu	Lys	Asn	Met	Tyr	Glu	Leu	Gln	Lys	Leu	Asn	Ser	Trp	Asp	Val
			20				25						30		
Phe	Gly	Asn													
		35													

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A
 /note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu	His	Arg	Ile	Asp	Leu	Gly	Pro	Pro	Ile	Ser	Leu	Glu	Arg	Leu	Asp
1				5					10					15	
Val	Gly	Thr	Asn	Leu	Gly	Asn	Ala	Ile	Ala	Lys	Leu	Glu	Ala	Lys	Glu
			20				25						30		

Leu Leu

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

His	Arg	Ile	Asp	Leu	Gly	Pro	Pro	Ile	Ser	Leu	Glu	Arg	Leu	Asp	Val
1				5					10					15	

Gly	Thr	Asn	Leu	Gly	Asn	Ala	Ile	Ala	Lys	Leu	Glu	Ala	Lys	Glu	Leu
			20					25					30		

Leu Glu

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

455

F

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Ile Asp Leu Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly
1 5 10 15
Thr Asn Leu Gly Asn Ala Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu
20 25 30
Glu Ser

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile Asp Leu Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr
1 5 10 15
Asn Leu Gly Asn Ala Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu Glu
20 25 30
Ser Ser

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asp Leu Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr Asn
1 5 10 15

Leu Gly Asn Ala Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu Glu Ser
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Leu Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr Asn Leu
1 5 10 15

Gly Asn Ala Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser
20 25 30

Asp Gln

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly
1 5 10 15

Asn Ala Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser Asp
20 25 30

Gln Ile

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl

group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly Asn
1 5 10 15

Ala Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser Asp Gln
20 25 30

Ile Leu

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= A

/note= "Preceding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /label= B

/note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly Asn Ala
1 5 10 15

Ile Ala Lys Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser Asp Gln Ile
20 25 30

Leu Arg

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A
 /note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly Asn Ala Ile Ala
 1 5 10 15

Lys Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser Asp Gln Ile Leu Arg
 20 25 30

Ser Met

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /label= A
 /note= "Preceeding this amino acid, there may be an amino group, a hydrophobic group, an acetyl group, a 9-fluorenylmethoxycarbonyl group, or a macromolecular carrier group."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /label= B
 /note= "Following this amino acid, there may be a carboxyl group, an amido group, a T-butyloxycarbonyl group, or a macromolecular carrier group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly Asn Ala Ile Ala Lys
 1 5 10 15

Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser Asp Gln Ile Leu Arg Ser
 20 25 30

Met Lys

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr
1 5 10 15
His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu
20 25

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser
1 5 10 15
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser
1 5 10 15
Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
20 25

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Leu Glu Lys Arg Arg Glu
 1 5 10 15
 Gln Leu Lys His Lys Leu Glu Gln Leu Arg Asn Ser
 20 25

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile Glu Lys Glu Phe Ser
 1 5 10 15
 Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr
 20 25

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu
 1 5 10 15
 Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu
 20 25 30
 Arg Tyr Leu Lys Asp Gln
 35

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala	Arg	Ser	1	5	10	15
Met	Thr	Leu	Thr	Val	Gln	Ala	Arg	Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	20	25	30	
Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Leu	Leu	35	40	45	
Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Ile	Leu	Ala	50	55	60	
Val	Glu	Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	65	70	75	
Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ala	Ser	Trp	85	90	95	
Ser	Asn	Lys	Ser	Leu	Glu	Gln	Ile	Trp	Asn	Asn	Met	Thr	Trp	Met	Glu	100	105	110	
Trp	Asp	Arg	Glu	Ile	Asn	Asn	Tyr	Thr	Ser	Leu	Ile	His	Ser	Leu	Ile	115	120	125	
Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu	Gln	Glu	Leu	Leu	Glu	130	135	140	
Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn	Trp	Phe	Asn	Ile	Thr	Asn	Trp	145	150	155	
Leu	Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Val	Gly	165	170	175	
Leu	Arg	Ile	Val	Phe	Ala	Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Gln	180	185	190	
Gly	Tyr	Ser	Pro	Leu	Ser	Phe	Gln	Thr	His	Leu	Pro	Thr	Pro	Arg	Gly	195	200	205	
Pro	Asp	Arg	Pro	Glu	Gly	Ile	Glu	Glu	Glu	Gly	Gly	Glu	Arg	Asp	Arg	210	215	220	
Asp	Arg	Ser	Ile	Arg	Leu	Val	Asn	Gly	Ser	Leu	Ala	Leu	Ile	Trp	Asp	225	230	235	
Asp	Leu	Arg	Ser	Leu	Cys	Leu	Phe	Ser	Tyr	His	Arg	Leu	Arg	Asp	Leu	245	250	255	
Leu	Leu	Ile	Val	Thr	Arg	Ile	Val	Glu	Leu	Leu	Gly	Arg	Arg	Gly	Trp	260	265	270	
Glu	Ala	Leu	Lys	Tyr	Trp	Trp	Asn	Leu	Leu	Gln	Tyr	Trp	Ser	Gln	Glu	275	280	285	
Leu	Lys	Asn	Ser	Ala	Val	Ser	Leu	Leu	Asn	Ala	Thr	Ala	Ile	Ala	Val	290	295	300	

Ala Glu Gly Thr Asp Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg
 305 310 315 320
 Ala Ile Arg His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile
 325 330 335
 Leu Leu

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val
 1 5 10 15
 Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys
 20 25 30
 Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly
 35 40 45
 Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp
 50 55 60
 Lys Gln Leu Leu Pro Ile Val Asn Lys Gln Ser Cys Ser Ile Ser Asn
 65 70 75 80
 Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu
 85 90 95
 Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser
 100 105 110
 Thr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
 115 120 125
 Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
 130 135 140
 Arg Gln Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu Val Leu
 145 150 155 160
 Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
 165 170 175
 Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
 180 185 190
 Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
 195 200 205
 Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
 210 215 220
 Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser

225		230		235		240
Glu Ile Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys						
	245			250		255
Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser						
	260			265		270
Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser						
	275			280		285
Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr						
	290			295		300
Val Ser Asn Lys Gly Met Asp Thr Val Ser Val Gly Asn Thr Leu Tyr						
	305			310		315
Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro						
	325			330		335
Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp						
	340			345		350
Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe						
	355			360		365
Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser						
	370			375		380
Thr Thr Asn Ile Met Ile Thr Thr Ile Ile Ile Val Ile Ile Val Ile						
	385			390		395
Leu Leu Ser Leu Ile Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg						
	405			410		415
Ser Thr Pro Val Thr Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn						
	420			425		430
Ile Ala Phe Ser Asn						
	435					

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Thr	Ala	Met	Gly	Ala	Ala	Ala
1				5					10					15	
Thr	Ala	Leu	Thr	Val	Gln	Ser	Gln	His	Leu	Leu	Ala	Gly	Ile	Leu	Gln
			20					25					30		
Gln	Gln	Lys	Asn	Leu	Leu	Ala	Ala	Val	Glu	Ala	Gln	Gln	Gln	Met	Leu
		35					40					45			
Lys	Leu	Thr	Ile	Trp	Gly	Val	Lys	Asn	Leu	Asn	Ala	Arg	Val	Thr	Ala
	50					55					60				

Leu Glu Lys Tyr Leu Glu Asp Gln Ala Arg Leu Asn Ala Trp Gly Cys
 65 70 75 80
 Ala Trp Lys Gln Val Cys His Thr Thr Val Pro Trp Gln Trp Asn Asn
 85 90 95
 Arg Thr Pro Asp Trp Asn Asn Met Thr Trp Leu Glu Trp Glu Arg Gln
 100 105 110
 Ile Ser Tyr Leu Glu Gly Asn Ile Thr Thr Gln Leu Glu Glu Ala Arg
 115 120 125
 Ala Gln Glu Glu Lys Asn Leu Asp Ala Tyr Gln Lys Leu Ser Ser Trp
 130 135 140
 Ser Asp Phe Trp Ser Trp Phe Asp Phe Ser Lys Trp Leu Asn Ile Leu
 145 150 155 160
 Lys Ile Gly Phe Leu Asp Val Leu Gly Ile Ile Gly Leu Arg Leu Leu
 165 170 175
 Tyr Thr Val Tyr Ser Cys Ile Ala Arg Val Arg Gln Gly Tyr Ser Pro
 180 185 190
 Leu Ser Pro Gln Ile His Ile His Pro Trp Lys Gly Gln Pro Asp Asn
 195 200 205
 Ala Glu Gly Pro Gly Glu Gly Gly Asp Lys Arg Lys Asn Ser Ser Glu
 210 215 220
 Pro Trp Gln Lys Glu Ser Gly Thr Ala Glu Trp Lys Ser Asn Trp Cys
 225 230 235 240
 Lys Arg Leu Thr Asn Trp Cys Ser Ile Ser Ser Ile Trp Leu Tyr Asn
 245 250 255
 Ser Cys Leu Thr Leu Leu Val His Leu Arg Ser Ala Phe Gln Tyr Ile
 260 265 270
 Gln Tyr Gly Leu Gly Glu Leu Lys Ala Ala Ala Gln Glu Ala Val Val
 275 280 285
 Ala Leu Ala Arg Leu Ala Gln Asn Ala Gly Tyr Gln Ile Trp Leu Ala
 290 295 300
 Cys Arg Ser Ala Tyr Arg Ala Ile Ile Asn Ser Pro Arg Arg Val Arg
 305 310 315 320
 Gln Gly Leu Glu Gly Ile Leu Asn
 325

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Phe Ala Gly Val Val Leu Ala Gly Val Ala Leu Gly Val Ala Thr Ala

1	5	10	15
Ala Gln Ile Thr 20	Ala Gly Ile Ala 25	Leu His Gln Ser Asn 30	Leu Asn Ala
Gln Ala Ile Gln Ser 35	Leu Arg Thr Ser 40	Leu Glu Gln Ser 45	Asn Lys Ala
Ile Glu Glu Ile Arg 50	Glu Ala Thr Gln 55	Glu Thr Val Ile 60	Ala Val Gln
Gly Val Gln Asp Tyr 65	Val Asn Asn Glu 70	Leu Val Pro Ala 75	Met Gln His 80
Met Ser Cys Glu 85	Leu Val Gly Gln 90	Arg Leu Gly Leu 95	Arg Leu Arg
Tyr Tyr Thr 100	Glu Leu Leu Ser 105	Ile Phe Gly Pro 110	Ser Leu Arg Asp Pro
Ile Ser Ala Glu 115	Ile Ser Ile Gln 120	Ala Leu Ile Tyr 125	Ala Leu Gly Gly
Glu Ile His Lys 130	Ile Leu Glu Lys 135	Leu Gly Tyr Ser 140	Gly Ser Asp Met
Ile Ala Ile Leu 145	Glu Ser Arg Gly 150	Ile Lys Thr Lys 155	Ile Thr His Val 160
Asp Leu Pro Gly 165	Lys Phe Ile Ile 170	Leu Ser Ile Ser 175	Tyr Pro Thr Leu
Ser Glu Val 180	Lys Gly Val Ile 185	Val His Arg Leu 190	Glu Ala Val Ser Tyr
Asn Ile Gly 195	Ser Gln Glu Trp 200	Tyr Thr Thr Val 205	Pro Arg Tyr Ile Ala
Thr Asn Gly 210	Tyr Leu Ile Ser 215	Asn Phe Asp Glu 220	Ser Ser Cys Val Phe
Val Ser Glu Ser 225	Ala Ile Cys Ser 230	Gln Asn Ser Leu 235	Tyr Pro Met Ser 240
Pro Leu Leu Gln 245	Gln Cys Ile Arg 250	Gly Asp Thr Ser 255	Ser Ser Cys Ala Arg
Thr Leu Val 260	Ser Gly Thr Met 265	Gly Asn Lys Phe 270	Ile Leu Ser Lys Gly
Asn Ile Val 275	Ala Asn Cys Ala 280	Ser Ile Leu Cys 285	Lys Cys Tyr Ser Thr
Ser Thr Ile 290	Ile Asn Gln Ser 295	Pro Asp Lys Leu 300	Leu Thr Phe Ile Ala
Ser Asp Thr 305	Cys Pro Leu Val 310	Glu Ile Asp Gly 315	Ala Thr Ile Gln Val 320
Gly Gly Arg Gln 325	Tyr Pro Asp Met 330	Val Tyr Glu Gly 335	Lys Val Ala Leu
Gly Pro Ala 340	Ile Ser Leu Asp 345	Arg Leu Asp Val 350	Gly Thr Asn Leu Gly
Asn Ala Leu 355	Lys Lys Leu Asp 360	Asp Ala Lys Val 365	Leu Ile Asp Ser Ser

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Asn Gln Ile Leu Glu Thr Val Arg Arg Ser Ser Phe Asn Phe Gly Ser
 370 375 380
 Leu Leu Ser Val Pro Ile Leu Ser Cys Thr Ala Leu Ala Leu Leu Leu
 385 390 395 400
 Leu Ile Tyr Cys Cys Lys Arg Arg Tyr Gln Gln Thr Leu Lys Gln His
 405 410 415
 Thr Lys Val Asp Pro Ala Phe Lys Pro Asp Leu Thr Gly Thr Ser Lys
 420 425 430
 Ser Tyr Val Arg Ser Leu
 435

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Phe Ile Gly Ala Ile Ile Gly Ser Val Ala Leu Gly Val Ala Thr Ala
 1 5 10 15
 Ala Gln Ile Thr Ala Ala Ser Ala Leu Ile Gln Ala Asn Gln Asn Ala
 20 25 30
 Ala Asn Ile Leu Arg Leu Lys Glu Ser Ile Thr Ala Thr Ile Glu Ala
 35 40 45
 Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala Val Ala Val Gly
 50 55 60
 Lys Met Gln Gln Phe Val Asn Asp Gln Phe Asn Asn Thr Ala Gln Glu
 65 70 75 80
 Leu Asp Cys Ile Lys Ile Thr Gln Gln Val Gly Val Glu Leu Asn Leu
 85 90 95
 Tyr Leu Thr Glu Leu Thr Thr Val Phe Gly Pro Gln Ile Thr Ser Pro
 100 105 110
 Ala Leu Thr Gln Leu Thr Ile Gln Ala Leu Tyr Asn Ala Gly Gly Asn
 115 120 125
 Met Asp Tyr Leu Leu Thr Lys Leu Gly Val Gly Asn Asn Gln Leu Ser
 130 135 140
 Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn Pro Ile Leu Tyr Asp
 145 150 155 160
 Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr Leu Pro Ser Val Gly
 165 170 175
 Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu Thr Leu Ser Val Ser
 180 185 190
 Thr Thr Lys Gly Phe Ala Ser Ala Leu Val Pro Lys Val Val Thr Gln

195					200					205					
Val	Gly	Ser	Val	Ile	Glu	Glu	Leu	Asp	Thr	Ser	Tyr	Cys	Ile	Glu	Thr
	210					215					220				
Asp	Leu	Asp	Leu	Tyr	Cys	Thr	Arg	Ile	Val	Thr	Phe	Pro	Met	Ser	Pro
225					230					235					240
Gly	Ile	Tyr	Ser	Cys	Leu	Asn	Gly	Asn	Thr	Ser	Ala	Cys	Met	Tyr	Ser
				245					250					255	
Lys	Thr	Glu	Gly	Ala	Leu	Thr	Thr	Pro	Tyr	Met	Thr	Leu	Lys	Gly	Ser
			260					265					270		
Val	Ile	Ala	Asn	Cys	Lys	Met	Thr	Thr	Cys	Arg	Cys	Ala	Asp	Pro	Pro
		275					280					285			
Gly	Ile	Ile	Ser	Gln	Asn	Tyr	Gly	Glu	Ala	Val	Ser	Leu	Ile	Asp	Arg
	290					295					300				
His	Ser	Cys	Asn	Val	Leu	Ser	Leu	Asp	Gly	Ile	Thr	Leu	Arg	Leu	Ser
305					310					315					320
Gly	Glu	Phe	Asp	Ala	Thr	Tyr	Gln	Lys	Asn	Ile	Ser	Ile	Leu	Asp	Ser
				325					330					335	
Gln	Val	Ile	Val	Thr	Gly	Asn	Leu	Asp	Ile	Ser	Thr	Glu	Leu	Gly	Asn
			340					345					350		
Val	Asn	Asn	Ser	Ile	Ser	Asn	Ala	Leu	Asp	Lys	Leu	Glu	Glu	Ser	Asn
		355					360					365			
Ser	Lys	Leu	Asp	Lys	Val	Asn	Val	Lys	Leu	Thr	Ser	Thr	Ser	Ala	Leu
	370					375					380				
Ile	Thr	Tyr	Ile	Ala	Leu	Thr	Ala	Ile	Ser	Leu	Val	Cys	Gly	Ile	Leu
385					390					395					400
Ser	Leu	Val	Leu	Ala	Cys	Tyr	Leu	Met	Tyr	Lys	Gln	Lys	Ala	Gln	Gln
				405					410					415	
Lys	Thr	Leu	Leu	Trp	Leu	Gly	Asn	Asn	Thr	Leu	Gly	Gln	Met	Arg	Ala
			420					425					430		
Thr	Thr	Lys	Met												
			435												

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Phe	Phe	Gly	Gly	Val	Ile	Gly	Thr	Ile	Ala	Leu	Gly	Val	Ala	Thr	Ser
1				5					10					15	
Ala	Gln	Ile	Thr	Ala	Ala	Val	Ala	Leu	Val	Glu	Ala	Lys	Gln	Ala	Arg
			20					25					30		

Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala
 35 40 45
 Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu Ile Val Ala Ile Lys
 50 55 60
 Ser Val Gln Asp Tyr Val Asn Lys Glu Ile Val Pro Ser Ile Ala Arg
 65 70 75 80
 Leu Gly Cys Glu Ala Ala Gly Leu Gln Leu Gly Ile Ala Leu Thr Gln
 85 90 95
 His Tyr Ser Glu Leu Thr Asn Ile Phe Gly Asp Asn Ile Gly Ser Leu
 100 105 110
 Gln Glu Lys Gly Ile Lys Leu Gln Gly Ile Ala Ser Leu Tyr Arg Thr
 115 120 125
 Asn Ile Thr Glu Ile Phe Thr Thr Ser Thr Val Asp Lys Tyr Asp Ile
 130 135 140
 Tyr Asp Leu Leu Phe Thr Glu Ser Ile Lys Val Arg Val Ile Asp Val
 145 150 155 160
 Asp Leu Asn Asp Tyr Ser Ile Thr Leu Gln Val Arg Leu Pro Leu Leu
 165 170 175
 Thr Arg Leu Leu Asn Thr Gln Ile Tyr Arg Val Asp Ser Ile Ser Tyr
 180 185 190
 Asn Ile Gln Asn Arg Glu Trp Tyr Ile Pro Leu Pro Ser His Ile Met
 195 200 205
 Thr Lys Gly Ala Phe Leu Gly Gly Ala Asp Val Lys Glu Cys Ile Glu
 210 215 220
 Ala Phe Ser Ser Tyr Ile Cys Pro Ser Asp Pro Gly Phe Val Leu Asn
 225 230 235 240
 His Glu Met Glu Ser Cys Leu Ser Gly Asn Ile Ser Gln Cys Pro Arg
 245 250 255
 Thr Val Val Lys Ser Asp Ile Val Pro Arg Tyr Ala Phe Val Asn Gly
 260 265 270
 Gly Val Val Ala Asn Cys Ile Thr Thr Thr Cys Thr Cys Asn Gly Ile
 275 280 285
 Gly Asn Arg Ile Asn Gln Pro Pro Asp Gln Gly Val Lys Ile Ile Thr
 290 295 300
 His Lys Glu Cys Asn Thr Ile Gly Ile Asn Gly Met Leu Phe Asn Thr
 305 310 315 320
 Asn Lys Glu Gly Thr Leu Ala Phe Tyr Thr Pro Asn Asp Ile Thr Leu
 325 330 335
 Asn Asn Ser Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn
 340 345 350
 Lys Ala Lys Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser
 355 360 365
 Asn Gln Lys Leu Asp Ser Ile Gly Asn Trp His Gln Ser Ser Thr Thr
 370 375 380
 Ile Ile Ile Val Leu Ile Met Ile Ile Ile Leu Phe Ile Ile Asn Val

385		390		395		400									
Thr	Ile	Ile	Ile	Ile	Ala	Val	Lys	Tyr	Tyr	Arg	Ile	Gln	Lys	Arg	Asn
				405					410					415	
Arg	Val	Asp	Gln	Asn	Asp	Lys	Pro	Tyr	Val	Leu	Thr	Asn	Lys		
			420					425					430		

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Asn	Gly	Trp	Glu	Gly
1				5					10					15	
Met	Ile	Asp	Gly	Trp	Tyr	Gly	Phe	Arg	His	Gln	Asn	Ser	Glu	Gly	Thr
			20					25					30		
Gly	Gln	Ala	Ala	Asp	Leu	Lys	Ser	Thr	Gln	Ala	Ala	Ile	Asp	Gln	Ile
		35					40					45			
Asn	Gly	Lys	Leu	Asn	Arg	Val	Ile	Glu	Lys	Thr	Asn	Glu	Lys	Phe	His
		50				55					60				
Gln	Ile	Glu	Lys	Glu	Phe	Ser	Glu	Val	Glu	Gly	Arg	Ile	Gln	Asp	Leu
65					70					75					80
Glu	Lys	Tyr	Val	Glu	Asp	Thr	Lys	Ile	Asp	Leu	Trp	Ser	Tyr	Asn	Ala
			85						90					95	
Glu	Leu	Leu	Val	Ala	Leu	Glu	Asn	Gln	His	Thr	Ile	Asp	Leu	Thr	Asp
			100					105					110		
Ser	Glu	Met	Asn	Lys	Leu	Phe	Glu	Lys	Thr	Arg	Arg	Gln	Leu	Arg	Glu
		115					120					125			
Asn	Ala	Glu	Glu	Met	Gly	Asn	Gly	Cys	Phe	Lys	Ile	Tyr	His	Lys	Cys
		130				135					140				
Asp	Asn	Ala	Cys	Ile	Glu	Ser	Ile	Arg	Asn	Gly	Thr	Tyr	Asp	His	Asp
145					150					155					160
Val	Tyr	Arg	Asp	Glu	Ala	Leu	Asn	Asn	Arg	Phe	Gln	Ile	Lys	Gly	Val
			165						170					175	
Glu	Leu	Lys	Ser	Gly	Tyr	Lys	Asp	Trp	Ile	Leu	Trp	Ile	Ser	Phe	Ala
			180					185					190		
Ile	Ser	Cys	Phe	Leu	Leu	Cys	Val	Val	Leu	Leu	Gly	Phe	Ile	Met	Trp
		195					200						205		
Ala	Cys	Gln	Arg	Gly	Asn	Ile	Arg	Cys	Asn	Ile	Cys	Ile			
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys
 1 5 10 15
 Cys Asn Gly Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr
 20 25 30
 Lys Asn Ala Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Ser Gly Val Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val
 1 5 10 15
 Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser
 20 25 30
 Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
 35 40 45
 Ile Asp Lys Gln Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp
 1 5 10 15

Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser
20 25 30
Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala
35 40 45
Gly Lys Ser Thr Thr
50

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Gly Thr Ile Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala
1 5 10 15
Val Ala Leu Val Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu
20 25 30
Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser
35 40 45
Ser Ile Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln Asp Tyr Val
50 55 60
Asn Lys Glu Ile Val Pro
65 70

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Tyr Thr Pro Asn Asp Ile Thr Leu Asn Asn Ser Val Ala Leu Asp Pro
1 5 10 15
Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu
20 25 30
Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile Gly
35 40 45
Asn Trp His Gln Ser Ser Thr Thr
50 55

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Arg	Asn	Lys	Arg	Gly	Val	Phe	Val	Leu	Gly	Phe	Leu	Gly	Phe	Leu	Ala	
1				5					10					15		
Thr	Ala	Gly	Ser	Ala	Met	Gly	Ala	Ala	Ser	Xaa	Xaa	Xaa	Xaa	Ala	Gln	
			20				25							30		
Ser	Arg	Thr	Leu	Leu	Ala	Gly	Ile	Val	Gln	Gln	Gln	Gln	Gln	Leu	Leu	
		35					40						45			
Asp	Val	Val	Lys	Arg	Gln	Gln	Glu	Leu	Leu	Arg	Leu	Thr	Val	Trp	Gly	
	50					55					60					
Thr	Lys	Asn	Leu	Gln	Thr	Arg	Val	Thr	Ala	Ile	Glu	Lys	Tyr	Leu	Lys	
65					70					75					80	
Asp	Gln	Ala	Gln	Leu	Asn	Ala	Trp	Gly	Cys	Ala	Phe	Arg	Gln	Val	Cys	
				85					90					95		
His	Thr	Thr	Val	Pro	Trp	Pro	Asn	Ala	Ser	Leu	Thr	Pro	Asp	Trp	Asn	
			100					105						110		
Asn	Asp	Thr	Trp	Gln	Glu	Trp	Glu	Arg	Lys	Val	Asp	Phe	Leu	Glu	Glu	
		115					120					125				
Asn	Ile	Thr	Ala	Leu	Leu	Glu	Glu	Ala	Gln	Ile	Gln	Gln	Glu	Lys	Asn	
	130					135					140					
Met	Tyr	Glu	Leu	Gln	Lys	Leu	Asn	Ser	Trp	Asp	Val	Phe	Gly	Asn	Xaa	
145					150					155					160	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				165					170						175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Tyr	Ile	Val	Met	Leu	
			180					185					190			
Ala	Lys	Leu	Arg	Gln	Gly	Tyr	Arg	Pro	Val	Phe	Ser	Ser	Pro	Pro	Ser	
		195					200					205				
Tyr	Phe	Gln	Xaa	Thr	His	Thr	Gln	Gln	Asp	Pro	Ala	Leu	Pro	Thr	Arg	
	210					215					220					
Glu	Gly	Lys	Glu	Gly	Asp	Gly	Gly	Glu	Gly	Gly	Gly	Asn	Ser	Ser	Trp	
225					230					235					240	
Pro	Trp	Gln	Ile	Glu	Tyr	Ile	His	Phe								
				245												

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

474

F

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met	Thr	Arg	Arg	Arg	Val	Leu	Ser	Val	Val	Val	Leu	Leu	Ala	Ala	Leu	
1				5					10					15		
Ala	Cys	Arg	Leu	Gly	Ala	Gln	Thr	Pro	Glu	Gln	Pro	Ala	Pro	Pro	Ala	
			20					25					30			
Thr	Thr	Val	Gln	Pro	Thr	Ala	Thr	Arg	Gln	Gln	Thr	Ser	Phe	Pro	Phe	
		35					40					45				
Arg	Val	Cys	Glu	Leu	Ser	Ser	His	Gly	Asp	Leu	Phe	Arg	Phe	Ser	Ser	
	50					55					60					
Asp	Ile	Gln	Cys	Pro	Ser	Phe	Gly	Thr	Arg	Glu	Asn	His	Thr	Glu	Gly	
65					70					75					80	
Leu	Leu	Met	Val	Phe	Lys	Asp	Asn	Ile	Ile	Pro	Tyr	Ser	Phe	Lys	Val	
			85						90					95		
Arg	Ser	Tyr	Thr	Lys	Ile	Val	Thr	Asn	Ile	Leu	Ile	Tyr	Asn	Gly	Trp	
			100					105					110			
Tyr	Ala	Asp	Ser	Val	Thr	Asn	Arg	His	Glu	Glu	Lys	Phe	Ser	Val	Asp	
		115					120					125				
Ser	Tyr	Glu	Thr	Asp	Gln	Met	Asp	Thr	Ile	Tyr	Gln	Cys	Tyr	Asn	Ala	
	130					135					140					
Val	Lys	Met	Thr	Lys	Asp	Gly	Leu	Thr	Arg	Val	Tyr	Val	Asp	Arg	Asp	
145					150					155					160	
Gly	Val	Asn	Ile	Thr	Val	Asn	Leu	Lys	Pro	Thr	Gly	Gly	Leu	Ala	Asn	
			165						170					175		
Gly	Val	Arg	Arg	Tyr	Ala	Ser	Gln	Thr	Glu	Leu	Tyr	Asp	Ala	Pro	Gly	
			180					185					190			
Trp	Leu	Ile	Trp	Thr	Tyr	Arg	Thr	Arg	Thr	Thr	Val	Asn	Cys	Leu	Ile	
		195					200					205				
Thr	Asp	Met	Met	Ala	Lys	Ser	Asn	Ser	Pro	Phe	Asp	Phe	Phe	Val	Thr	
	210					215					220					
Thr	Thr	Gly	Gln	Thr	Val	Glu	Met	Ser	Pro	Phe	Tyr	Asp	Gly	Lys	Asn	
225					230					235					240	
Lys	Glu	Thr	Phe	His	Glu	Arg	Ala	Asp	Ser	Phe	His	Val	Arg	Thr	Asn	
			245						250					255		
Tyr	Lys	Ile	Val	Asp	Tyr	Asp	Asn	Arg	Gly	Thr	Asn	Pro	Gln	Gly	Glu	
			260					265					270			
Arg	Arg	Ala	Phe	Leu	Asp	Lys	Gly	Thr	Tyr	Thr	Leu	Ser	Trp	Lys	Leu	
		275					280					285				
Glu	Asn	Arg	Thr	Ala	Tyr	Cys	Pro	Leu	Gln	His	Trp	Gln	Thr	Phe	Asp	
	290					295					300					
Ser	Thr	Ile	Ala	Thr	Glu	Thr	Gly	Lys	Ser	Ile	His	Phe	Val	Thr	Asp	

305						310						315					320
Glu	Gly	Thr	Ser	Ser	Phe	Val	Thr	Asn	Thr	Thr	Val	Gly	Ile	Glu	Leu		
				325					330					335			
Pro	Asp	Ala	Phe	Lys	Cys	Ile	Glu	Glu	Gln	Val	Asn	Lys	Thr	His	Glu		
			340					345					350				
Lys	Tyr	Glu	Ala	Val	Gln	Asp	Arg	Tyr	Thr	Lys	Gly	Gln	Glu	Ala	Ile		
		355					360					365					
Thr	Tyr	Phe	Ile	Thr	Ser	Gly	Gly	Leu	Leu	Leu	Ala	Trp	Leu	Pro	Leu		
	370					375					380						
Thr	Pro	Arg	Ser	Leu	Ala	Thr	Val	Lys	Asn	Leu	Thr	Glu	Leu	Thr	Thr		
	385				390					395					400		
Pro	Thr	Ser	Ser	Pro	Pro	Ser	Ser	Pro	Ser	Pro	Pro	Ala	Pro	Ser	Ala		
				405					410					415			
Ala	Arg	Gly	Ser	Thr	Pro	Ala	Ala	Val	Leu	Arg	Arg	Arg	Arg	Arg	Asp		
			420					425					430				
Ala	Gly	Asn	Ala	Thr	Thr	Pro	Val	Pro	Pro	Thr	Ala	Pro	Gly	Lys	Ser		
		435					440					445					
Leu	Gly	Thr	Leu	Asn	Asn	Pro	Ala	Thr	Val	Gln	Ile	Gln	Phe	Ala	Tyr		
	450					455					460						
Asp	Ser	Leu	Arg	Arg	Gln	Ile	Asn	Arg	Met	Leu	Gly	Asp	Leu	Ala	Arg		
	465				470				475						480		
Ala	Trp	Cys	Leu	Glu	Gln	Lys	Arg	Gln	Asn	Met	Val	Leu	Arg	Glu	Leu		
			485						490					495			
Thr	Lys	Ile	Asn	Pro	Thr	Thr	Val	Met	Ser	Ser	Ile	Tyr	Gly	Lys	Ala		
			500					505					510				
Val	Ala	Ala	Lys	Arg	Leu	Gly	Asp	Val	Ile	Ser	Val	Ser	Gln	Cys	Val		
		515					520					525					
Pro	Val	Asn	Gln	Ala	Thr	Val	Thr	Leu	Arg	Lys	Ser	Met	Arg	Val	Pro		
	530					535					540						
Gly	Ser	Glu	Thr	Met	Cys	Tyr	Ser	Arg	Pro	Leu	Val	Ser	Phe	Ser	Phe		
	545				550					555					560		
Ile	Asn	Asp	Thr	Lys	Thr	Tyr	Glu	Gly	Gln	Leu	Gly	Thr	Asp	Asn	Glu		
				565					570					575			
Ile	Phe	Leu	Thr	Lys	Lys	Met	Thr	Glu	Val	Cys	Gln	Ala	Thr	Ser	Gln		
			580					585					590				
Tyr	Tyr	Phe	Gln	Ser	Gly	Asn	Glu	Ile	His	Val	Tyr	Asn	Asp	Tyr	His		
		595					600					605					
His	Phe	Lys	Thr	Ile	Glu	Leu	Asp	Gly	Ile	Ala	Thr	Leu	Gln	Thr	Phe		
	610					615					620						
Ile	Ser	Leu	Asn	Thr	Ser	Leu	Ile	Glu	Asn	Ile	Asp	Phe	Ala	Ser	Leu		
	625				630					635					640		
Glu	Leu	Tyr	Ser	Arg	Asp	Glu	Gln	Arg	Ala	Ser	Asn	Val	Phe	Asp	Leu		
				645					650					655			
Glu	Gly	Ile	Phe	Arg	Glu	Tyr	Asn	Phe	Gln	Ala	Gln	Asn	Ile	Ala	Gly		
			660					665					670				

Leu Arg Lys Asp Leu Asp Asn Ala Val Ser Asn Gly Arg Asn Gln Phe
 675 680 685
 Val Asp Gly Leu Gly Glu Leu Met Asp Ser Leu Gly Ser Val Gly Gln
 690 695 700
 Ser Ile Thr Asn Leu Val Ser Thr Val Gly Gly Leu Phe Ser Ser Leu
 705 710 715 720
 Val Ser Gly Phe Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met Leu
 725 730 735
 Ile Leu Val Leu Val Ala Gly Val Val Ile Leu Val Ile Ser Leu Thr
 740 745 750
 Arg Arg Thr Arg Gln Met Ser Gln Gln Pro Val Gln Met Leu Tyr Pro
 755 760 765
 Gly Ile Asp Glu Leu Ala Gln Gln His Ala Ser Gly Glu Gly Pro Gly
 770 775 780
 Ile Asn Pro Ile Ser Lys Thr Glu Leu Gln Ala Ile Met Leu Ala Leu
 785 790 795 800
 His Glu Gln Asn Gln Glu Gln Lys Arg Ala Ala Gln Arg Ala Ala Gly
 805 810 815
 Pro Ser Val Ala Ser Arg Ala Leu Gln Ala Ala Arg Asp Arg Phe Pro
 820 825 830
 Gly Leu Arg Arg Arg Arg Tyr His Asp Pro Glu Thr Ala Ala Ala Leu
 835 840 845
 Leu Gly Glu Ala Glu Thr Glu Phe
 850 855

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Met Asp Pro Asn Ser Thr Ser Glu Asp Val Lys Phe Thr Pro Asp
 1 5 10 15
 Pro Tyr Gln Val Pro Phe Val Gln Ala Phe Asp Gln Ala Thr Arg Val
 20 25 30
 Tyr Gln Asp Leu Gly Gly Pro Ser Gln Ala Pro Leu Pro Cys Val Leu
 35 40 45
 Trp Pro Val Leu Pro Glu Pro Leu Pro Gln Gly Gln Leu Thr Ala Tyr
 50 55 60
 His Val Ser Thr Ala Pro Thr Gly Ser Trp Phe Ser Ala Pro Gln Pro
 65 70 75 80
 Ala Pro Glu Asn Ala Tyr Gln Ala Tyr Ala Ala Pro Gln Leu Phe Pro

85										90					95															
Val	Ser	Asp	Ile	Thr	Gln	Asn	Gln	Gln	Thr	Asn	Gln	Ala	Gly	Gly	Glu															
			100					105					110																	
Ala	Pro	Gln	Pro	Gly	Asp	Asn	Ser	Thr	Val	Gln	Thr	Ala	Ala	Ala	Val															
		115					120					125																		
Val	Phe	Ala	Cys	Pro	Gly	Ala	Asn	Gln	Gly	Gln	Gln	Leu	Ala	Asp	Ile															
	130					135					140																			
Gly	Val	Pro	Gln	Pro	Ala	Pro	Val	Ala	Ala	Pro	Ala	Arg	Arg	Thr	Arg															
145					150					155					160															
Lys	Pro	Gln	Gln	Pro	Glu	Ser	Leu	Glu	Glu	Cys	Asp	Ser	Glu	Leu	Glu															
				165				170						175																
Ile	Lys	Arg	Tyr	Lys	Asn	Arg	Val	Ala	Ser	Arg	Lys	Cys	Arg	Ala	Lys															
			180					185					190																	
Phe	Lys	Gln	Leu	Leu	Gln	His	Tyr	Arg	Glu	Val	Ala	Ala	Ala	Lys	Ser															
		195					200					205																		
Ser	Glu	Asn	Asp	Arg	Leu	Arg	Leu	Leu	Leu	Lys	Gln	Met	Cys	Pro	Ser															
	210					215					220																			
Leu	Asp	Val	Asp	Ser	Ile	Ile	Pro	Arg	Thr	Pro	Asp	Val	Leu	His	Glu															
225					230					235					240															
Asp	Leu	Leu	Asn	Phe																										
				245																										

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 438 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Phe	Ala	Gly	Val	Val	Leu	Ala	Gly	Ala	Ala	Leu	Gly	Val	Ala	Thr	Ala															
1				5					10					15																
Ala	Gln	Ile	Thr	Ala	Gly	Ile	Ala	Leu	His	Gln	Ser	Met	Leu	Asn	Ser															
			20				25						30																	
Gln	Ala	Ile	Asp	Asn	Leu	Arg	Ala	Ser	Leu	Glu	Thr	Thr	Asn	Gln	Ala															
		35				40						45																		
Ile	Glu	Ala	Ile	Arg	Gln	Ala	Gly	Gln	Glu	Met	Ile	Leu	Ala	Val	Gln															
	50				55				60																					
Gly	Val	Gln	Asp	Tyr	Ile	Asn	Asn	Glu	Leu	Ile	Pro	Ser	Met	Asn	Gln															
65					70				75					80																
Leu	Ser	Cys	Asp	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Leu	Lys	Leu	Leu	Arg															
				85					90					95																
Tyr	Tyr	Thr	Glu	Ile	Leu	Ser	Leu	Phe	Gly	Pro	Ser	Leu	Arg	Asp	Pro															
			100					105					110																	

Ile	Ser	Ala	Glu	Ile	Ser	Ile	Gln	Ala	Leu	Ser	Tyr	Ala	Leu	Gly	Gly		
		115					120					125					
Asp	Ile	Asn	Lys	Val	Leu	Glu	Lys	Leu	Gly	Tyr	Ser	Gly	Gly	Asp	Leu		
	130					135					140						
Leu	Gly	Ile	Leu	Glu	Ser	Arg	Gly	Ile	Lys	Ala	Arg	Ile	Thr	His	Val		
	145				150					155					160		
Asp	Thr	Glu	Ser	Tyr	Phe	Ile	Val	Leu	Ser	Ile	Ala	Tyr	Pro	Thr	Leu		
				165					170					175			
Ser	Glu	Ile	Lys	Gly	Val	Ile	Val	His	Arg	Leu	Glu	Gly	Val	Ser	Tyr		
			180					185					190				
Asn	Ile	Gly	Ser	Gln	Glu	Trp	Tyr	Thr	Thr	Val	Pro	Lys	Tyr	Val	Ala		
		195					200					205					
Thr	Gln	Gly	Tyr	Leu	Ile	Ser	Asn	Phe	Asp	Glu	Ser	Ser	Cys	Thr	Phe		
	210					215					220						
Met	Pro	Glu	Gly	Thr	Val	Cys	Ser	Gln	Asn	Ala	Leu	Tyr	Pro	Met	Ser		
	225				230					235					240		
Pro	Leu	Leu	Gln	Glu	Cys	Leu	Arg	Gly	Ser	Thr	Lys	Ser	Cys	Ala	Arg		
			245						250					255			
Thr	Leu	Val	Ser	Gly	Ser	Phe	Gly	Asn	Arg	Phe	Ile	Leu	Ser	Gln	Gly		
		260						265					270				
Asn	Leu	Ile	Ala	Asn	Cys	Ala	Ser	Ile	Leu	Cys	Lys	Cys	Tyr	Thr	Thr		
	275						280					285					
Gly	Thr	Ile	Ile	Asn	Gln	Asp	Pro	Asp	Lys	Ile	Leu	Thr	Tyr	Ile	Ala		
	290					295					300						
Ala	Asp	His	Cys	Pro	Val	Val	Glu	Val	Asn	Gly	Val	Thr	Ile	Gln	Val		
	305				310					315					320		
Gly	Ser	Arg	Arg	Tyr	Pro	Asp	Ala	Val	Tyr	Leu	His	Arg	Ile	Asp	Leu		
				325					330					335			
Gly	Pro	Pro	Ile	Ser	Leu	Glu	Arg	Leu	Asp	Val	Gly	Thr	Asn	Leu	Gly		
			340					345					350				
Asn	Ala	Ile	Ala	Lys	Leu	Glu	Asp	Ala	Lys	Glu	Leu	Leu	Glu	Ser	Ser		
	355						360					365					
Asp	Gln	Ile	Leu	Arg	Ser	Met	Lys	Gly	Leu	Ser	Ser	Thr	Ser	Ile	Val		
	370					375					380						
Tyr	Ile	Leu	Ile	Ala	Val	Cys	Leu	Gly	Gly	Leu	Ile	Gly	Ile	Pro	Ala		
	385				390					395					400		
Leu	Ile	Cys	Cys	Cys	Arg	Gly	Arg	Cys	Asn	Lys	Lys	Gly	Glu	Gln	Val		
				405					410					415			
Gly	Met	Ser	Arg	Pro	Gly	Leu	Lys	Pro	Asp	Leu	Thr	Gly	Thr	Ser	Lys		
			420					425					430				
Ser	Tyr	Val	Arg	Ser	Leu												
					435												

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Gly	Gln	Asn	Leu	Ser	Thr	Ser	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	
1				5					10					15		
His	Gln	Leu	Asp	Pro	Ala	Phe	Arg	Ala	Asn	Thr	Ala	Asn	Pro	Asp	Trp	
			20					25					30			
Asp	Phe	Asn	Pro	Asn	Lys	Asp	Thr	Trp	Pro	Asp	Ala	Asn	Lys	Val	Gly	
		35					40					45				
Ala	Gly	Ala	Phe	Gly	Leu	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	
	50					55					60					
Gly	Trp	Ser	Pro	Gln	Ala	Gln	Gly	Ile	Leu	Gln	Thr	Leu	Pro	Ala	Asn	
65				70						75					80	
Pro	Pro	Pro	Ala	Ser	Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	
				85					90					95		
Leu	Ser	Pro	Pro	Leu	Arg	Asn	Thr	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	
			100					105					110			
Ser	Thr	Thr	Phe	His	Gln	Thr	Leu	Gln	Asp	Pro	Arg	Val	Arg	Gly	Leu	
		115					120					125				
Tyr	Phe	Pro	Ala	Gly	Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Leu	
	130					135					140					
Thr	Thr	Ala	Ser	Pro	Leu	Ser	Ser	Ile	Phe	Ser	Arg	Ile	Gly	Asp	Pro	
145					150					155					160	
Ala	Leu	Asn	Met	Glu	Asn	Ile	Thr	Ser	Gly	Phe	Leu	Gly	Pro	Leu	Leu	
				165					170					175		
Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu	Thr	Arg	Ile	Leu	Thr	Ile	Pro	
			180					185					190			
Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	Leu	Asn	Phe	Leu	Gly	Gly	Thr	
		195					200					205				
Thr	Val	Cys	Leu	Gly	Gln	Asn	Ser	Gln	Ser	Pro	Thr	Ser	Asn	His	Ser	
	210					215					220					
Pro	Thr	Ser	Cys	Pro	Pro	Thr	Cys	Pro	Gly	Tyr	Arg	Trp	Met	Cys	Leu	
225					230					235					240	
Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	
				245					250					255		
Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	
			260					265					270			
Ile	Pro	Gly	Ser	Ser	Thr	Thr	Ser	Thr	Gly	Pro	Cys	Arg	Thr	Cys	Met	
		275					280					285				
Thr	Thr	Ala	Gln	Gly	Thr	Ser	Met	Tyr	Pro	Ser	Cys	Cys	Cys	Thr	Lys	
	290					295					300					

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
 305 310 315 320
 Phe Gly Lys Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu
 325 330 335
 Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
 340 345 350
 Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
 355 360 365
 Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
 370 375 380
 Leu Trp Val Tyr Ile
 385

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Ala Ile Gln Leu Ile Pro Leu Phe Val Gly Leu Gly Ile Thr Thr Ala
 1 5 10 15
 Val Ser Thr Gly Ala Ala Gly Leu Gly Val Ser Ile Thr Gln Tyr Thr
 20 25 30
 Lys Leu Ser His Gln Leu Ile Ser Asp Val Gln Ala Ile Ser Ser Thr
 35 40 45
 Ile Gln Asp Leu Gln Asp Gln Val Asp Ser Leu Ala Glu Val Val Leu
 50 55 60
 Gln Asn Arg Arg Gly Leu Asp Leu Leu Thr Ala Glu Gln Gly Gly Ile
 65 70 75 80
 Cys Leu Ala Leu Gln Glu Lys Cys Cys Phe Tyr Ala Asn Lys Ser Gly
 85 90 95
 Ile Val Arg Asp Lys Ile Lys Asn Leu Gln Asp Asp Leu Glu Arg Arg
 100 105 110
 Arg Arg Gln Leu Ile Asp Asn Pro Phe Trp Thr Ser Phe His Gly Phe
 115 120 125
 Leu Pro Tyr Val Met Pro Leu Leu Gly Pro Leu Leu Cys Leu Leu Leu
 130 135 140
 Val Leu Ser Phe Gly Pro Ile Ile Phe Asn Lys Leu Met Thr Phe Ile
 145 150 155 160
 Lys His Gln Ile Glu Ser Ile Gln Ala Lys Pro Ile Gln Val His Tyr
 165 170 175
 His Arg Leu Glu Gln Glu Asp Ser Gly Gly Ser Tyr Leu Thr Leu Thr

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Lys Ala Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile Val Val
 1             5             10
Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Ile Pro Gln Tyr Gln Asp
 20             25             30
Tyr Thr Ala Arg Thr Gln Val Thr Arg Ala Val Ser Glu Val Ser Ala
 35             40             45
Leu Lys Thr Ala Ala Glu Ser Ala Ile Leu Glu Gly Lys Glu Ile Val
 50             55             60
Ser Ser Ala Thr Pro Lys Asp Thr Gln Tyr Asp Ile Gly Phe Thr Glu
 65             70             75             80
Ser Thr Leu Leu Asp Gly Ser Gly Lys Ser Gln Ile Gln Val Thr Asp
 85             90             95
Asn Gln Asp Gly Thr Val Glu Leu Val Ala Thr Leu Gly Lys Ser Ser
 100            105            110
Gly Ser Ala Ile Lys Gly Ala Val Ile Thr Val Ser Arg Lys Asn Asp
 115            120            125
Gly Val Trp Asn Cys Lys Ile Thr Lys Thr Pro Thr Ala Trp Lys Pro
 130            135            140
Asn Tyr Ala Pro Ala Asn Cys Pro Lys Ser
 145            150

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Asn Thr Leu Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile Val
 1             5             10             15
Ile Ala Ile Val Gly Ile Leu Ala Ala Val Ala Leu Pro Ala Tyr Gln

```

20										25					30							
Asp	Tyr	Thr	Ala	Arg	Ala	Gln	Val	Ser	Glu	Ala	Ile	Leu	Leu	Ala	Glu							
		35					40					45										
Gly	Gln	Lys	Ser	Ala	Val	Thr	Glu	Tyr	Tyr	Leu	Asn	His	Gly	Ile	Trp							
	50					55					60											
Pro	Lys	Asp	Asn	Thr	Ser	Ala	Gly	Val	Ala	Ser	Ser	Ser	Ser	Ile	Lys							
	65				70					75					80							
Gly	Lys	Tyr	Val	Lys	Glu	Val	Lys	Val	Glu	Asn	Gly	Val	Val	Thr	Ala							
				85					90					95								
Thr	Met	Asn	Ser	Ser	Asn	Val	Asn	Lys	Glu	Ile	Gln	Gly	Lys	Lys	Leu							
			100					105					110									
Ser	Leu	Trp	Ala	Lys	Arg	Gln	Asp	Gly	Ser	Val	Lys	Trp	Phe	Cys	Gly							
		115					120					125										
Gln	Pro	Val	Thr	Arg	Asn	Ala	Lys	Asp	Asp	Thr	Val	Thr	Ala	Asp	Ala							
		130				135						140										
Thr	Gly	Asn	Asp	Gly	Lys	Ile	Asp	Thr	Lys	His	Leu	Pro	Ser	Thr	Cys							
	145				150					155					160							
Arg	Asp	Asn	Phe	Asp	Ala	Ser																
						165																

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Lys	Lys	Thr	Leu	Leu	Gly	Ser	Leu	Ile	Leu	Leu	Ala	Phe	Ala	Gly				
1				5					10				15						
Asn	Val	Gln	Ala	Asp	Ile	Asn	Thr	Glu	Thr	Ser	Gly	Lys	Val	Thr	Phe				
		20						25				30							
Phe	Gly	Lys	Val	Val	Glu	Asn	Thr	Cys	Lys	Val	Lys	Thr	Glu	His	Lys				
		35					40					45							
Asn	Leu	Ser	Val	Val	Leu	Asn	Asp	Val	Gly	Lys	Asn	Ser	Leu	Ser	Thr				
		50				55					60								
Lys	Val	Asn	Thr	Ala	Met	Pro	Thr	Pro	Phe	Thr	Ile	Thr	Leu	Gln	Asn				
	65				70					75				80					
Cys	Asp	Pro	Thr	Thr	Ala	Asn	Gly	Thr	Ala	Asn	Lys	Ala	Asn	Lys	Val				
				85					90					95					
Gly	Leu	Tyr	Phe	Tyr	Ser	Trp	Lys	Asn	Val	Asp	Lys	Glu	Asn	Asn	Phe				
			100					105					110						
Thr	Leu	Lys	Asn	Glu	Gln	Thr	Thr	Ala	Asp	Tyr	Ala	Thr	Asn	Val	Asn				
		115					120					125							

Ile Gln Leu Met Glu Ser Asn Gly Thr Lys Ala Ile Ser Val Val Gly
130 135 140

Lys Glu Thr Glu Asp Phe Met His Thr Asn Asn Asn Gly Val Ala Leu
145 150 155 160

Asn Gln Thr His Pro Asn Asn Ala His Ile Ser Gly Ser Thr Gln Leu
165 170 175

Thr Thr Gly Thr Asn Glu Leu Pro Leu His Phe Ile Ala Gln Tyr Tyr
180 185 190

Ala Thr Asn Lys Ala Thr Ala Gly Lys Val Gln Ser Ser Val Asp Phe
195 200 205

Gln Ile Ala Tyr Glu
210

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Asn Lys Lys Leu Leu Met Asn Phe Phe Ile Val Ser Pro Leu Leu
1 5 10 15

Leu Ala Thr Thr Ala Thr Asp Phe Thr Pro Val Pro Leu Ser Ser Asn
20 25 30

Gln Ile Ile Lys Thr Ala Lys Ala Ser Thr Asn Asp Asn Ile Lys Asp
35 40 45

Leu Leu Asp Trp Tyr Ser Ser Gly Ser Asp Thr Phe Thr Asn Ser Glu
50 55 60

Val Leu Asp Asn Ser Leu Gly Ser Met Arg Ile Lys Asn Thr Asp Gly
65 70 75 80

Ser Ile Ser Leu Ile Ile Phe Pro Ser Pro Tyr Tyr Ser Pro Ala Phe
85 90 95

Thr Lys Gly Glu Lys Val Asp Leu Asn Thr Lys Arg Thr Lys Lys Ser
100 105 110

Gln His Thr Ser Glu Gly Thr Tyr Ile His Phe Gln Ile Ser Gly Val
115 120 125

Thr Asn Thr Glu Lys Leu Pro Thr Pro Ile Glu Leu Pro Leu Lys Val
130 135 140

Lys Val His Gly Lys Asp Ser Pro Leu Lys Tyr Gly Pro Lys Phe Asp
145 150 155 160

Lys Lys Gln Leu Ala Ile Ser Thr Leu Asp Phe Glu Ile Arg His Gln
165 170 175

Leu Thr Gln Ile His Gly Leu Tyr Arg Ser Ser Asp Lys Thr Gly Gly

	180		185		190
Tyr Trp Lys Ile Thr Met Asn Asp Gly Ser Thr Tyr Gln Ser Asp Leu					
195			200		205
Ser Lys Lys Phe Glu Tyr Asn Thr Glu Lys Pro Pro Ile Asn Ile Asp					
210		215		220	
Glu Ile Lys Thr Ile Glu Ala Glu Ile Asn					
225	230				

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Lys Lys Thr Ala Phe Ile Leu Leu Leu Phe Ile Ala Leu Thr Leu					
1	5		10		15
Thr Thr Ser Pro Leu Val Asn Gly Ser Glu Lys Ser Glu Glu Ile Asn					
	20		25		30
Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Arg Asn Ala Leu Ser					
	35		40		45
Asn Leu Arg Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Ile Thr Glu Asn					
	50		55		60
Lys Glu Ser Asp Asp Gln Phe Leu Glu Asn Thr Leu Leu Phe Lys Gly					
65	70		75		80
Phe Phe Thr Gly His Pro Trp Tyr Asn Asp Leu Leu Val Asp Leu Gly					
	85		90		95
Ser Lys Asp Ala Thr Asn Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr					
	100		105		110
Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr					
	115		120		125
Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr					
	130		135		140
Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Ile Asp Gly Lys Gln Thr					
145	150		155		160
Thr Val Pro Ile Asp Lys Val Lys Thr Ser Lys Lys Glu Val Thr Val					
	165		170		175
Gln Glu Leu Asp Leu Gln Ala Arg His Tyr Leu His Gly Lys Phe Gly					
	180		185		190
Leu Tyr Asn Ser Asp Ser Phe Gly Gly Lys Val Gln Arg Gly Leu Ile					
	195		200		205
Val Phe His Ser Ser Glu Gly Ser Thr Val Ser Tyr Asp Leu Phe Asp					
	210		215		220

Ala Gln Gly Gln Tyr Pro Asp Thr Leu Leu Arg Ile Tyr Arg Asp Asn
 225 230 235 240
 Lys Thr Ile Asn Ser Glu Asn Leu His Ile Asp Leu Tyr Leu Tyr Thr
 245 250 255
 Thr

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Lys Lys Thr Ala Phe Thr Leu Leu Leu Phe Ile Ala Leu Thr Leu
 1 5 10 15
 Thr Thr Ser Pro Leu Val Asn Gly Ser Glu Lys Ser Glu Glu Ile Asn
 20 25 30
 Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Thr Ala Leu Gly
 35 40 45
 Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
 50 55 60
 Lys Glu Ser His Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly
 65 70 75 80
 Phe Phe Thr Asp His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp
 85 90 95
 Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr
 100 105 110
 Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr
 115 120 125
 Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr
 130 135 140
 Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
 145 150 155 160
 Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val
 165 170 175
 Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn
 180 185 190
 Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile
 195 200 205
 Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
 210 215 220
 Ala Gln Gly Gln Tyr Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn

Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
245 250

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met	Met	Phe	Ser	Gly	Phe	Asn	Ala	Asp	Tyr	Glu	Ala	Ser	Ser	Ser	Arg	1	5	10	15
Cys	Ser	Ser	Ala	Ser	Pro	Ala	Gly	Asp	Ser	Leu	Ser	Tyr	Tyr	His	Ser	20	25	30	
Pro	Ala	Asp	Ser	Phe	Ser	Ser	Met	Gly	Ser	Pro	Val	Asn	Ala	Gln	Asp	35	40	45	
Phe	Cys	Thr	Asp	Leu	Ala	Val	Ser	Ser	Ala	Asn	Phe	Ile	Pro	Thr	Val	50	55	60	
Thr	Ala	Ile	Ser	Thr	Ser	Pro	Asp	Leu	Gln	Trp	Leu	Val	Gln	Pro	Ala	65	70	75	80
Leu	Val	Ser	Ser	Val	Ala	Pro	Ser	Gln	Thr	Arg	Ala	Pro	His	Pro	Phe	85	90	95	
Gly	Val	Pro	Ala	Pro	Ser	Ala	Gly	Ala	Tyr	Ser	Arg	Ala	Gly	Val	Val	100	105	110	
Lys	Thr	Met	Thr	Gly	Gly	Arg	Ala	Gln	Ser	Ile	Gly	Arg	Arg	Gly	Lys	115	120	125	
Val	Glu	Gln	Leu	Ser	Pro	Glu	Glu	Glu	Glu	Lys	Arg	Arg	Ile	Arg	Arg	130	135	140	
Glu	Arg	Asn	Lys	Met	Ala	Ala	Ala	Lys	Cys	Arg	Asn	Arg	Arg	Arg	Glu	145	150	155	160
Leu	Thr	Asp	Thr	Leu	Gln	Ala	Glu	Thr	Asp	Gln	Leu	Glu	Asp	Glu	Lys	165	170	175	
Ser	Ala	Leu	Gln	Thr	Glu	Ile	Ala	Asn	Leu	Leu	Lys	Glu	Lys	Glu	Lys	180	185	190	
Leu	Glu	Phe	Ile	Leu	Ala	Ala	His	Arg	Pro	Ala	Cys	Lys	Ile	Pro	Asp	195	200	205	
Asp	Leu	Gly	Phe	Pro	Glu	Glu	Met	Ser	Val	Ala	Ser	Leu	Asp	Leu	Thr	210	215	220	
Gly	Gly	Leu	Pro	Glu	Val	Ala	Thr	Pro	Glu	Ser	Glu	Glu	Ala	Phe	Thr	225	230	235	240
Leu	Pro	Leu	Leu	Asn	Asp	Pro	Glu	Pro	Lys	Pro	Ser	Val	Glu	Pro	Val	245	250	255	
Lys	Ser	Ile	Ser	Ser	Met	Glu	Leu	Lys	Thr	Glu	Pro	Phe	Asp	Asp	Phe				

260	265	270
Leu Phe Pro Ala Ser Ser Arg Pro Ser Gly Ser Glu Thr Ala Arg Ser		
275	280	285
Val Pro Asp Met Asp Leu Ser Gly Ser Phe Tyr Ala Leu Pro Leu Leu		
290	295	300
Asn Asp Pro Glu Pro Lys Pro Ser Val Glu Pro Val Lys Ser Ile Ser		
305	310	315
Ser Met Glu Leu Lys Thr Glu Pro Phe Asp Asp Phe Leu Phe Pro Ala		
325	330	335
Ser Ser Arg Pro Ser Gly Ser Glu Thr Ala Arg Ser Val Pro Asp Met		
340	345	350
Asp Leu Ser Gly Ser Phe Tyr Ala Gly Ser Ser Ser Asn Glu Pro Ser		
355	360	365
Ser Asp Ser Leu Ser Ser Pro Thr Leu Leu Ala Leu		
370	375	380

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Ser Gly Trp Glu Ser Tyr Tyr Lys Thr Glu Gly Asp Glu Glu Ala Glu	
1	15
Glu Glu Gln Glu Glu Asn Leu Glu Ala Ser Gly Asp Tyr Lys Tyr Ser	
20	30
Gly Arg Asp Ser Leu Ile Phe Leu Val Asp Ala Ser Lys Ala Met Phe	
35	45
Glu Ser Gln Ser Glu Asp Glu Leu Thr Pro Phe Asp Met Ser Ile Gln	
50	60
Cys Ile Gln Ser Val Tyr Ile Ser Lys Ile Ile Ser Ser Asp Arg Asp	
65	80
Leu Leu Ala Val Val Phe Tyr Gly Thr Glu Lys Asp Lys Asn Ser Val	
85	95
Asn Phe Lys Asn Ile Tyr Val Leu Gln Glu Leu Asp Asn Pro Gly Ala	
100	110
Lys Arg Ile Leu Glu Leu Asp Gln Phe Lys Gly Gln Gln Gly Gln Lys	
115	125
Arg Phe Gln Asp Met Met Gly His Gly Ser Asp Tyr Ser Leu Ser Glu	
130	140
Val Leu Trp Val Cys Ala Asn Leu Phe Ser Asp Val Gln Phe Lys Met	
145	160

Ser His Lys Arg Ile Met Leu Phe Thr Asn Glu Asp Asn Pro His Gly
 165 170 175
 Asn Asp Ser Ala Lys Ala Ser Arg Ala Arg Thr Lys Ala Gly Asp Leu
 180 185 190
 Arg Asp Thr Gly Ile Phe Leu Asp Leu Met His Leu Lys Lys Pro Gly
 195 200 205
 Gly Phe Asp Ile Ser Leu Phe Tyr Arg Asp Ile Ile Ser Ile Ala Glu
 210 215 220
 Asp Glu Asp Leu Arg Val His Phe Glu Glu Ser Ser Lys Leu Glu Asp
 225 230 235 240
 Leu Leu Arg Lys Val Arg Ala Lys Glu Thr Arg Lys Arg Ala Leu Ser
 245 250 255
 Arg Leu Lys Leu Lys Leu Asn Lys Asp Ile Val Ile Ser Val Gly Ile
 260 265 270
 Tyr Asn Leu Val Gln Lys Ala Leu Lys Pro Pro Pro Ile Lys Leu Tyr
 275 280 285
 Arg Glu Thr Asn Glu Pro Val Lys Thr Lys Thr Arg Thr Phe Asn Thr
 290 295 300
 Ser Thr Gly Gly Leu Leu Leu Pro Ser Asp Thr Lys Arg Ser Gln Ile
 305 310 315 320
 Tyr Gly Ser Arg Gln Ile Ile Leu Glu Lys Glu Glu Thr Glu Glu Leu
 325 330 335
 Lys Arg Phe Asp Asp Pro Gly Leu Met Leu Met Gly Phe Lys Pro Leu
 340 345 350
 Val Leu Leu Lys Lys His His Leu Arg Pro Ser Leu Phe Val Tyr Pro
 355 360 365
 Glu Glu Ser Leu Val Ile Gly Ser Ser Thr Leu Phe Ser Ala Leu Leu
 370 375 380
 Ile Lys Cys Leu Glu Lys Glu Val Ala Ala Leu Cys Arg Tyr Thr Pro
 385 390 395 400
 Arg Arg Asn Ile Pro Pro Tyr Phe Val Ala Leu Val Pro Gln Glu Glu
 405 410 415
 Glu Leu Asp Asp Gln Lys Ile Gln Val Thr Pro Pro Gly Phe Gln Leu
 420 425 430
 Val Phe Leu Pro Phe Ala Asp Asp Lys Arg Lys Met Pro Phe Thr Glu
 435 440 445
 Lys Ile Met Ala Thr Pro Glu Gln Val Gly Lys Met Lys Ala Ile Val
 450 455 460
 Glu Lys Leu Arg Phe Thr Tyr Arg Ser Asp Ser Phe Glu Asn Pro Val
 465 470 475 480
 Leu Gln Gln His Phe Arg Asn Leu Glu Ala Leu Ala Leu Asp Leu Met
 485 490 495
 Glu Pro Glu Gln Ala Val Asp Leu Thr Leu Pro Lys Val Glu Ala Met
 500 505 510
 Asn Lys Arg Leu Gly Ser Leu Val Asp Glu Phe Lys Glu Leu Val Tyr

515		520		525
Pro Pro Asp Tyr Asn Pro Glu Gly Lys Val Thr Lys Arg Lys His Asp	530	535	540	
Asn Glu Gly Ser Gly Ser Lys Arg Pro Lys Val Glu Tyr Ser Glu Glu	545	550	555	560
Glu Leu Lys Thr His Ile Ser Lys Gly Thr Leu Gly Lys Phe Thr Val	565	570	575	
Pro Met Leu Lys Glu Ala Cys Arg Ala Tyr Gly Leu Lys Ser Gly Leu	580	585	590	
Lys Lys Gln Glu Leu Leu Glu Ala Leu Thr Lys His Phe Gln Asp	595	600	605	

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gly Gly Gly Ala Leu Ser Pro Gln His Ser Ala Val Thr Gln Gly Ser	1	5	10	15
Ile Ile Lys Asn Lys Glu Gly Met Asp Ala Lys Ser Leu Thr Ala Trp	20	25	30	
Ser Arg Thr Leu Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg	35	40	45	
Glu Glu Trp Lys Leu Leu Asp Thr Ala Gln Gln Ile Val Tyr Arg Asn	50	55	60	
Val Met Leu Glu Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln Leu	65	70	75	80
Thr Lys Pro Asp Val Ile Leu Arg Leu Glu Lys Gly Glu Glu Pro Trp	85	90	95	
Leu Val Glu Arg Glu Ile His Gln Glu Thr His Pro Asp Ser Glu Thr	100	105	110	
Ala Phe Glu Ile Lys Ser Ser Val Ser Ser Arg Ser Ile Phe Lys Asp	115	120	125	
Lys Gln Ser Cys Asp Ile Lys Met Glu Gly Met Ala Arg Asn Asp Leu	130	135	140	
Trp Tyr Leu Ser Leu Glu Glu Val Trp Lys Cys Arg Asp Gln Leu Asp	145	150	155	160
Lys Tyr Gln Glu Asn Pro Glu Arg His Leu Arg His Gln Leu Ile His	165	170	175	
Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser				

Pro Asp Ala Val Tyr Leu His Arg Ile Asp Leu Gly Pro Pro Ile Ser
 1 5 10 15
 Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly Asn Ala Ile Ala Lys
 20 25 30
 Leu Glu Asp
 35

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly Asn Ala Ile Ala Lys
 1 5 10 15
 Leu Glu Ala Lys Glu Leu Leu Glu Ser Ser Asp Gln Ile Leu Arg Ser
 20 25 30
 Met Lys

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Thr Trp Gln Glu Trp Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile
 1 5 10 15
 Thr Ala Leu Leu Glu Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr
 20 25 30
 Glu Leu Gln Lys Leu Asn Ser Trp Asp Val Phe Gly Asn Trp Phe
 35 40 45

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala
1 5 10 15
Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val
20 25 30
Thr Glu Leu Gln Leu Leu Met Gln Ser Thr
35 40

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Val Ser Lys Gly Tyr Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val
1 5 10 15
Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn
20 25

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "X represents U, the standard designation for C-abu, a modified cysteine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys
1 5 10 15

Xaa Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp
20 25 30

Lys Tyr Lys
35

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "X represents U, the standard designation for C-abu, a modified cysteine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Xaa
1 5 10 15

Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys
20 25 30

Tyr Lys Asn
35

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "X represents U, the standard designation for C-abu, a modified cysteine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Xaa Asn

1 5 10 15
 Gly Thr Asp Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr
 20 25 30
 Lys Asn Ala
 35

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "X represents U, the standard designation for C-abu, a modified cysteine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ser Asn Ile Lys Glu Asn Lys Xaa Asn Gly Thr Asp Ala Lys Val Lys
 1 5 10 15
 Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu
 20 25 30
 Gln Leu Leu
 35

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "X represents U, the standard designation for C-abu, a modified cysteine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Glu Asn Lys Xaa Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 1 5 10 15
 Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
 20 25 30
 Met Gln Ser
 35

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "X represents U, the standard designation for C-abu, a modified cysteine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr
1 5 10 15
Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Xaa Asn
20 25 30
Gly Thr Asp Ala
35

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu
1 5 10 15
Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu
20 25

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser

Leu Ser Asn Gly Val
35

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu
1 5 10 15
Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu
20 25 30
Thr Ser Lys
35

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln
1 5 10 15
Gln Ser Tyr Ser Ile Met Ser Ile Ile Lys Glu Glu
20 25

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn
1 5 10 15
Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr

20

25

30

Thr Pro Val Ser
35

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe
1 5 10 15

Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala
20 25 30

Phe Ile Arg
35

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Leu
1 5 10 15

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val
20 25

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly
1 5 10 15

Lys Ser Thr

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu
1 5 10 15

Ala Phe Ile

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn
1 5 10 15

Ala Gly Lys Ser Thr
 20

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu
1 5 10 15

Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly
 20 25 30

Lys

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
1 5 10 15
Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser
 20 25 30
Thr

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu
1 5 10 15
Ala Phe Ile Arg Lys Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly
 20 25 30
Lys Ser Thr
 35

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu Val Glu Ala Lys
1 5 10 15

Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala
20 25

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Ala Ala Val Ala Leu Val Glu Ala Lys Gln Ala Arg Ser Asp Ile Glu
1 5 10 15
Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val
20 25 30
Gln Ser Ser
35

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Ala Lys Gln Ala Arg Ser Asp Ile Glu Lys Leu Lys Glu Ala Ile Arg
1 5 10 15
Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly Asn Leu
20 25 30
Ile Val Ala
35

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Ile Arg Asp Thr Asn Lys Ala Val Gln Ser Val Gln Ser Ser Ile Gly

1	5	10	15
Asn	Leu	Ile	Val
	Ala	Ile	Lys
	Ser	Val	Gln
		Asp	Tyr
	20	25	

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala	Val	Gln	Ser	Val	Gln	Ser	Ser	Ile	Gly	Asn	Leu	Ile	Val	Ala	Ile
1				5					10					15	
Lys	Ser	Val	Gln	Asp	Tyr	Val	Asn	Lys	Glu	Ile	Val				
			20					25							

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Leu	Lys	Glu	Ala	Ile	Arg	Asp	Thr	Asn	Lys	Ala	Val	Gln	Ser	Val	Gln
1				5					10					15	
Ser	Ser	Ile	Gly	Asn	Leu	Ile	Val	Ala	Ile	Lys	Ser				
			20					25							

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Glu	Trp	Ile	Arg	Arg	Ser	Asn	Gln	Lys	Leu	Asp	Ser	Ile
1				5					10			

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys Ser Asp Leu Glu Glu
 1 5 10 15
 Ser Lys Glu Trp Ile Lys Lys Ser Asn Gln Lys Leu Asp Ser Ile Gly
 20 25 30
 Asn Trp His
 35

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Leu
 1 5 10 15
 Glu Trp Ile Arg Arg Ser Asn Gln Lys Leu Asp Ser Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Asp Gln Gln Ile Lys Gln Tyr Lys Arg Leu Leu Asp Arg Leu Ile Ile
 1 5 10 15
 Pro Leu Tyr Asp Gly Leu Arg Gln Lys Asp Val Ile Val Ser Asn Gln
 20 25 30
 Glu Ser Asn
 35

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Tyr Ser Glu Leu Thr Asn Ile Phe Gly Asp Asn Ile Gly Ser Leu Gln
1 5 10 15
Glu Lys Gly Ile Lys Leu Gln Gly Ile Ala Ser Leu Tyr Arg Thr Asn
20 25 30
Ile Thr Glu Ile
35

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Thr Ser Ile Thr Leu Gln Val Arg Leu Pro Leu Leu Thr Arg Leu Leu
1 5 10 15
Asn Thr Gln Ile Tyr Arg Val Asp Ser Ile Ser Tyr Asn Ile Gln Asn
20 25 30
Arg Glu Trp Tyr
35

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp
1 5 10 15
Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu

20

25

30

Glu Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp
 35 40 45

Lys Trp Ala Ser Leu Trp Asn Trp Phe
 50 55

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile Gly
 1 5 10 15

Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu
 20 25 30

Leu Leu Glu
 35

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
 1 5 10 15

Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30

Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Leu Ile Lys Ile Phe
 35 40 45

Ile

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Glu Ala Ala Ala Arg Glu Ala Ala Ala Arg Glu Ala Ala Ala Arg Leu
1 5 10 15

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
20 25

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Leu
1 5 10 15

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
20 25

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Phe Trp Asn Trp Leu Ser Ala Trp Lys Asp Leu Glu Leu Lys Ser Leu
1 5 10 15

Leu Glu Glu Val Lys Asp Glu Leu Gln Lys Met Arg
20 25

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn
1 5 10 15
Tyr His Leu Glu Asn Glu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp
20 25 30
Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Phe Trp Asn Trp Leu Ser Ala Trp Lys Asp Leu Glu Leu Tyr Pro Gly
1 5 10 15
Ser Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Cys Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Cys Leu Glu Leu Asp Lys Trp Ala Ser Leu Ala Asn Trp Phe Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn	Phe	Phe	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Ala	Asn	Ala	Phe
1				5					10			

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Phe	Asn	Phe	Phe
1				5					10			

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Ala Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Leu Glu Leu Asp Lys Trp Ala Ser Ala Trp Asn Trp Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu Glu Leu Asp Lys Ala Ala Ser Leu Trp Asn Trp Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Leu Lys Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Leu Glu Leu Lys Lys Trp Ala Ser Leu Trp Asn Trp Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Cys Gly Gly Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln
1 5 10 15

Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp
20 25 30

Ala Ser Leu Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
 1 5 10 15
 Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30
 Trp Asn Ala Phe
 35

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
 1 5 10 15
 Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30
 Ala Asn Trp Phe
 35

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
 1 5 10 15
 Glu Lys Asn Glu Gln Gln Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30
 Trp Asn Trp Phe
 35

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Gln Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Gln Gln Glu Leu Leu Gln Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Tyr Thr Ser Leu Ile Gln Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Gln Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asn Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Gln Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Tyr Thr Ser Leu Ile His Ser Leu Ile Gln Glu Ser Gln Asn Gln Gln
 1 5 10 15
 Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30
 Trp Asn Trp Phe
 35

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Tyr Thr Ser Leu Ile His Ser Leu Ile Gln Gln Ser Gln Asn Gln Gln
 1 5 10 15
 Gln Lys Asn Gln Gln Gln Leu Leu Gln Leu Asp Lys Trp Ala Ser Leu
 20 25 30
 Trp Asn Trp Phe
 35

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
 1 5 10 15
 Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
 20 25 30

Ala Asn Ala Ala
35

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Gln Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Tyr Thr Ser Leu Ile Gln Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Gln Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln

1	5	10	15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu			
20		25	30
Phe Asn Phe Phe			
35			

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Leu Gln			
1	5	10	15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu			
20		25	30
Trp Asn Trp Phe			
35			

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln			
1	5	10	15
Glu Lys Leu Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu			
20		25	30
Trp Asn Trp Phe			
35			

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Phe Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Pro Ala Ser Leu
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Pro
20 25 30
Trp Asn Trp Phe
35

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln
1 5 10 15
Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30
Trp Asn Ser Phe
35

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Leu Leu Asp Asn Phe Glu Ser Thr Trp Glu Gln Ser Lys Glu Leu Trp
1 5 10 15
Glu Gln Gln Glu Ile Ser Ile Gln Asn Leu His Lys Ser Ala Leu Gln
20 25 30
Glu Tyr Trp Asn
35

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Leu Ser Asn Leu Leu Gln Ile Ser Asn Asn Ser Asp Glu Trp Leu Glu
1 5 10 15
Ala Leu Glu Ile Glu His Glu Lys Trp Lys Leu Thr Gln Trp Gln Ser
20 25 30
Tyr Glu Gln Phe
35

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
1 5 10 15
Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
20 25 30
Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
35 40 45
Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ser Glu Leu Glu Ile Lys Arg Tyr Lys Asn Arg Val Ala Ser Arg Lys
1 5 10 15
Cys Arg Ala Lys Phe Gln Leu Leu Gln His Tyr Arg Glu Val Ala Ala
20 25 30
Ala Lys Ser Ser Glu Asn Asp Arg Leu Arg Leu Leu Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ala Ser Arg Lys Cys Arg Ala Lys Phe Lys Gln Leu Leu Gln His Tyr
1 5 10 15
Arg Glu Val Ala Ala Ala Lys Ser Ser Glu Asn Asp Arg Leu Arg Leu

20

25

30

Leu Leu Lys Gln Met Cys Pro Ser Leu Asp Val Asp Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Leu Leu Gln His Tyr Arg Glu Val Ala Ala Ala Lys Ser Ser Glu Asn
 1 5 10 15

Asp Arg Leu Arg Leu Leu Lys Gln Met Cys Pro Ser Leu Asp Val
 20 25 30

Asp Ser Ile
 35

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Leu Gln His Tyr Arg Glu Val Ala Ala Ala Lys Ser Ser Glu Asn Asp
 1 5 10 15

Arg Leu Arg Leu Leu Leu Lys Gln Met Cys Pro Ser Leu Asp Val Asp
 20 25 30

Ser Ile Ile Pro Arg Thr Pro Asp Val Leu His Glu Asp
 35 40 45

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

522

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Ser Ser Glu Asn Asp Arg Leu Arg Leu Leu Leu Lys Gln Met Cys Pro
 1 5 10 15
 Ser Leu Asp Val Asp Ser Ile Ile Pro Arg Thr Pro Asp Val Leu His
 20 25 30
 Glu Asp Leu
 35

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Ser Glu Asn Asp Arg Leu Arg Leu Leu Leu Lys Gln Met Cys Pro Ser
 1 5 10 15
 Leu Asp Val Asp Ser Ile Ile Pro Arg Thr Pro Asp Val Leu His Glu
 20 25 30
 Asp Leu Leu Asn Phe
 35

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
 1 5 10 15
 Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
 20 25 30
 Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser Pro
 35 40 45

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe
1 5 10 15
Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln
20 25 30
Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Ser Thr
35 40 45
Gly Pro Cys Arg Thr Cys Met Thr Thr
50 55

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Xaa Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys
1 5 10 15
Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp
20 25 30
Lys Tyr Lys Asn Xaa
35

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Xaa	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile	Lys	Glu	Asn	Lys	Cys
1				5					10					15	
Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys	Gln	Glu	Leu	Asp	Lys
			20					25					30		
Tyr	Lys	Asn	Ala	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Xaa	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile	Lys	Glu	Asn	Lys	Cys	Asn
1				5					10					15	
Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys	Gln	Glu	Leu	Asp	Lys	Tyr
			20					25					30		

Lys Asn Ala Val Xaa
35

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Xaa	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys
1				5					10					15	
Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly
			20					25					30		
Val	Ser	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35

526 F

(D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
Xaa Ala Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile
 1           5           10           15
Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val
          20           25           30
Ser Val Xaa
      35
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
Xaa Val Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala
 1           5           10           15
Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser
          20           25           30
Val Leu Xaa
      35
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

Xaa Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu
 1           5           10          15
Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val
          20          25          30
Leu Thr Xaa
          35

```

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

Xaa Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu Leu
 1           5           10          15
Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu
          20          25          30
Thr Ser Xaa

```

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F

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Xaa	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys
1				5					10					15	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			20					25					30		
Leu	Asp	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl

group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Xaa	Gly	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val
1				5				10						15	
Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp
			20					25					30		
Leu	Lys	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Xaa	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val
1				5				10						15	
Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu
			20					25					30		
Lys	Asn	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

Xaa Val Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
 1           5           10          15
Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys
          20          25          30
Asn Tyr Xaa
          35

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

Xaa Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu
 1           5           10          15
Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn
          20          25          30
Tyr Ile Xaa
          35

```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Xaa	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser
1				5				10					15		
Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr
			20					25					30		
Ile	Asp	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited

to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Xaa	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn
1				5					10					15	
Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile
			20					25					30		
Asp	Lys	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Xaa	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly
1				5					10					15	
Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp
			20					25					30		
Lys	Gln	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino

group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Xaa	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys
1				5					10					15	
Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly
			20					25					30		
Val	Ser	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Xaa	Ala	Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile
1				5					10					15	
Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val
			20					25					30		
Ser	Val	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Xaa	Val	Ser	Lys	Val	Leu	His	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Ala
1				5					10					15	
Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser
			20					25					30		
Val	Leu	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Xaa Ser Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu
1 5 10 15
Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val
20 25 30
Leu Thr Xaa
35

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Xaa Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Ala Leu Leu
1 5 10 15
Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu
20 25 30
Thr Ser Xaa
35

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group;

a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Xaa	Leu	Glu	Gly	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys
1				5					10					15	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			20					25					30		
Leu	Asp	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Xaa	Gly	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val
1				5				10					15		
Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp
			20					25				30			
Leu	Lys	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids

537

F

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Xaa	Glu	Val	Asn	Lys	Ile	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val
1			5						10					15	
Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu
			20					25					30		
Lys	Asn	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Xaa Val Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
1 5 10 15
Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys
20 25 30
Asn Tyr Xaa
35

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Xaa Asn Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu
1 5 10 15
Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn
20 25 30
Tyr Ile Xaa
35

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited

to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```
Xaa Lys Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser
 1           5           10           15
Asn Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr
          20           25           30
Ile Asp Xaa
          35
```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```
Xaa Ile Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser Leu Ser Asn
 1           5           10           15
Gly Val Ser Val Leu Thr Ser Lys Val Leu Asp Leu Lys Asn Tyr Ile
          20           25           30
Asp Lys Xaa
          35
```

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION:/note="Xaa may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Xaa	Ala	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Val	Val	Ser	Leu	Ser	Asn	Gly
1				5				10						15	
Val	Ser	Val	Leu	Thr	Ser	Lys	Val	Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp
			20					25					30		
Lys	Gln	Xaa													
		35													

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 49
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Xaa	Pro	Leu	Leu	Val	Leu	Gln	Ala	Gly	Phe	Phe	Leu	Leu	Thr	Arg	Ile
1				5				10						15	
Leu	Thr	Ile	Pro	Gln	Ser	Leu	Asp	Ser	Trp	Trp	Thr	Ser	Leu	Asn	Phe
			20					25					30		

Leu Gly Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser Pro
 35 40 45
 Xaa

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Xaa Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile
 1 5 10 15
 Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe
 20 25 30
 Leu Gly Gly Thr Xaa
 35

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Xaa Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu

1	5	10	15
Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu			
	20	25	30
Gly Gly Thr Thr Xaa			
35			

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Xaa Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr			
1	5	10	15
Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly			
	20	25	30
Gly Thr Thr Val Xaa			
35			

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Xaa Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
 1 5 10 15
 Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Gly Leu Gly Gly Thr
 20 25 30
 Thr Val Cys Leu Xaa
 35

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Xaa Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
 1 5 10 15
 Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr
 20 25 30
 Val Cys Leu Gly Xaa
 35

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Xaa Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
 1 5 10 15
 Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val
 20 25 30
 Cys Leu Gly Gln Xaa
 35

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Xaa Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
 1 5 10 15
 Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys
 20 25 30
 Leu Gly Gln Asn Xaa
 35

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Xaa Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
 1 5 10 15
 Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu
 20 25 30
 Gly Gln Asn Ser Xaa
 35

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Xaa Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 1 5 10 15
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly
 20 25 30
 Gln Asn Ser Gln Xaa
 35

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Xaa Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
 1 5 10 15
 Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln
 20 25 30
 Asn Ser Gln Ser Xaa
 35

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 59
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Xaa Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
 1 5 10 15
 Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
 20 25 30
 Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Ser
 35 40 45
 Thr Gly Pro Cys Arg Thr Cys Met Thr Thr Xaa
 50 55

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Xaa Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
1 5 10 15
Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
20 25 30
Gln Gly Met Leu Xaa
35

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Xaa Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe
1 5 10 15
Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln
20 25 30
Gly Met Leu Pro Xaa
35

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Xaa Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile
1 5 10 15
Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly
20 25 30
Met Leu Pro Val Xaa
35

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Xaa	Arg	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu
1				5					10					15	
Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met
		20						25					30		
Leu	Pro	Val	Cys	Xaa											
		35													

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Xaa	Trp	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu
1				5					10					15	
Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu
		20						25					30		
Pro	Val	Cys	Pro	Xaa											
		35													

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Xaa	Met	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu
1				5					10				15		
Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro
			20					25					30		
Val	Cys	Pro	Ile	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Xaa	Cys	Leu	Arg	Arg	Phe	Ile	Ile	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys
1				5				10				15			
Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val
			20					25				30			
Cys	Pro	Leu	Ile	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Xaa Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
 1           5           10          15
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
      20           25           30
Pro Leu Ile Pro Xaa
      35

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Xaa Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
 1           5           10          15
Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
      20           25           30
Leu Ile Pro Gly Xaa
      35

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```
Xaa Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
 1           5           10          15
Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
      20           25          30
Ile Pro Gly Ser Xaa
      35
```

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```
Xaa Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
 1           5           10          15
Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile
      20           25          30
Gly Gly Ser Ser Xaa
      35
```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```
Xaa Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
 1           5           10           15
Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro
 20           25           30
Gly Ser Ser Thr Xaa
 35
```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```
Xaa Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
 1           5           10           15
Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
 20           25           30
Ser Ser Thr Ser Xaa
 35
```

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Xaa	Phe	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu
1				5				10						15	
Leu	Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser
			20					25					30		
Ser	Thr	Ser	Thr	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Xaa	Leu	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu
1				5				10					15		
Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser
			20					25					30		
Thr	Ser	Thr	Gly	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Xaa	Phe	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp
1			5						10					15	
Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser	Thr
			20					25					30		
Ser	Thr	Gly	Pro	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Xaa	Ile	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr
1			5						10					15	
Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser	Thr	Ser
			20					25					30		
Thr	Gly	Pro	Cys	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Xaa	Leu	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln
1				5				10					15		
Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser	Thr	Ser	Thr
			20					25					30		
Gly	Pro	Cys	Arg	Xaa											
		35													

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Xaa	Leu	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly
1				5				10					15		
Met	Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser	Thr	Ser	Thr	Gly
			20					25					30		
Pro	Cys	Arg	Thr	Xaa											
		35													

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Xaa	Leu	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met
1				5					10					15	
Leu	Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser	Thr	Ser	Thr	Gly	Pro
			20					25						30	
Cys	Arg	Thr	Cys	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Xaa	Cys	Leu	Ile	Phe	Leu	Leu	Val	Leu	Leu	Asp	Tyr	Gln	Gly	Met	Leu
1				5					10					15	
Pro	Val	Cys	Pro	Leu	Ile	Pro	Gly	Ser	Ser	Thr	Ser	Thr	Gly	Pro	Cys
			20					25					30		
Arg	Thr	Cys	Met	Xaa											
			35												

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Xaa Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro
1 5 10 15
Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Ser Thr Gly Pro Cys Arg
20 25 30
Thr Cys Met Thr Xaa
35

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note="Xaa comprises an amino group, an acetyl group, a 9-fluorenylmethoxy-carbonyl group, a hydrophobic group, or a macromolecule carrier group.

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION:/note="Xaa comprises a carboxyl group, an amido group, a hydrophobic group, or a macromolecular carrier group for an effective period of time so that no infection of the cell by the virus occurs.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Xaa Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
1 5 10 15
Cys Pro Leu Ile Pro Gly Ser Ser Thr Ser Thr Gly Pro Cys Arg Thr
20 25 30
Cys Met Thr Thr Xaa
35